

REMARKS

Claims 1-12 and 15 are pending in the present Application. Reconsideration and allowance of the claims are respectfully requested in view of the following remarks.

Claim Rejections Under 35 U.S.C. § 112, First Paragraph

Claims 12 stands rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement. Reciting that the computer readable medium is not a carrier wave is deemed to be new matter. Applicants respectfully traverse this rejection.

Claim 12 is drawn to a computer readable medium having embodied thereon a computer program comprising computer readable code for executing a method, wherein the computer readable medium is not a carrier wave.

Applicants assert that the limitation “wherein the computer readable medium is not a carrier wave” is not new matter. In the specification at p. 12, lines 29-33, Applicants disclose a genus “computer readable medium” and a number of species within that genus, including carrier waves. As carrier waves are disclosed as one of a number of possible species within the genus “computer readable medium”, the limitation “wherein the computer readable medium is not a carrier wave” merely claims less than the full scope of the disclosure for the Applicants, which the courts have determined is a perfectly legitimate procedure since it is for an inventor to decide what bounds of protection he will seek. *In re Johnson*, 558 F.2d 1008, 194 U.S.P.Q. 187 (C.C.P.A. 1977), is authority for the proposition that if the Applicant has a genus and some species, Applicant is able to claim the genus minus the disclosed species. In this case, the CCPA noted that Johnson was simply claiming less than the full scope of his disclosure, a perfectly legitimate procedure since it is for an inventor to decide what bounds of protection he will seek. Thus, this case illustrates that an inventor may excise prior art from a claimed genus. Similarly, Applicants can explicitly exclude a species recited in the disclosure which is currently viewed by the courts and the USPTO as nonstatutory subject matter and still satisfy the written description requirement of § 112, first paragraph.

Applicants therefore request reconsideration and withdrawal of the rejection of claim 12 under §112, first paragraph.

Claim Rejections Under 35 U.S.C. § 103(a)

Claims 1-12 and 15 stand rejected under 35 U.S.C. § 103(a), as being unpatentable over Benson et al. (Nucleic Acids Research, 1999, Vol. 27, pages 38-43). Applicants respectfully traverse this rejection.

For an obviousness rejection to be proper, the Examiner must meet the burden of establishing that all elements of the invention are disclosed in the prior art; that the prior art relied upon, or knowledge generally available in the art at the time of the invention, must provide some suggestion or incentive that would have motivated the skilled artisan to modify a reference or combined references. *In re Fine*, 5 U.S.P.Q.2d 1596, 1598 (Fed. Cir. 1988). “A patent composed of several elements is not proved obvious merely by demonstrating that each of its elements was, independently, known in the prior art.” *KSR Int’l Co. v. Teleflex Inc.*, 127 S.Ct. 1727, 1741 (2007). To find obviousness, the Examiner must “identify a reason that would have prompted a person of ordinary skill in the art in the relevant field to combine the elements in the way the claimed new invention does.” *Id.*

The claimed invention is drawn to a system and method for determining a location of a target sequence in a genome sequence, and to a computer readable medium having embodied thereon a computer program comprising computer readable code for executing the method.

Claim 1 is drawn to a system for determining a location of a target sequence in a genome sequence, comprising: a storage unit for storing a crosslink map, wherein the crosslink map comprises records of sequence information for a plurality of versions of a genome sequence; an information search unit, for searching for identifier information and sequence information corresponding to a target sequence among the records in the crosslink map; and a location estimation unit, for determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; and determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value.

Claim 7 is drawn to a method of determining a location of a target sequence in a genome sequence, the method comprising: inputting a target sequence; searching for identifier

information and sequence information corresponding to the target sequence in a crosslink map, wherein the crosslink map comprises records of sequence information for a plurality of versions of a genome sequence; determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value; and outputting the location of the target sequence in the genome sequence to a user.

Claim 12 is drawn to a computer readable medium having embodied thereon a computer program comprising computer readable code for executing the method.

Benson et al. provide a general description of certain aspects of the GenBank® public database of nucleotide and protein sequences. (p. 12, 1st col., Introduction) Benson et al. describe the organization of GenBank; how the database is built by input of new sequences via one of two programs, Bankit or Sequin; and retrieving GenBank data using Entrez, BLAST, or other means such as anonymous FTP. However, Benson et al. are silent with respect to at least a crosslink map as recited in claim 7, wherein the crosslink map comprises records of sequence information for a plurality of versions of a genome sequence; determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; or determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value.

The Office Action states that Benson et al. teach tables, on p. 39, left column, that are interpreted as a crosslink map because they link the various sequence features with the locations in the sequences. However, in the passage pointed to on p. 39, left column, Benson et al. teaches that each GenBank entry includes a description of the sequence, the scientific name and taxonomy of the source organism, and “a table of features that identifies coding regions and other sites of biological significance”, as well as protein translations. The table of features taught by Benson et al. is stated to be for a single GenBank sequence entry. Therefore

it is not a crosslink map comprising records of sequence information for a plurality of versions of a genome sequence as recited in claim 7.

Further, while the Office Action states that BLAST uses a query sequence to search the entire database to find homologous sequences and locations of the query sequence in the sequences in the database, it does not cite anywhere in Benson et al. that the following limitations of claim 7 are taught: determining a reference group comprising a reference sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by more than a predetermined number of records; calculating a difference value of a start position and an end position of the reference sequence information obtained from the crosslink map; or determining a location of the target sequence in the genome sequence by a location shift corresponding to the difference value. Neither does the Office Action explain what general knowledge of one of skill in the art at the time the claimed invention was made supplements the teachings of Benson et al. that would render the method of claims 7-11 obvious. Thus, Applicants assert that the Office Action has failed to establish that claims 7-11 are obvious over Benson et al.

Furthermore, as Benson et al. fails to teach all limitations of the method of claim 7-11 as noted above, Benson et al. cannot teach all elements of the computer readable medium of claim 12 having embodied thereon a computer program comprising computer readable code for executing the method of claim 7, nor can Benson et al. teach all the functional limitations for components of the system of claims 1-6 and 15 for performing the method for determining a location of a target sequence in a genome sequence. Therefore Applicants assert that the Office Action also fails to establish that claims 1-6, 12, and 15 are obvious over Benson et al.

Applicants request reconsideration and withdrawal of the rejection of claims 1-12 and 15 under 35 U.S.C. § 103(a), as being obvious over Benson et al.

It is believed that the foregoing amendments and remarks fully comply with the Office Action and that the claims herein should now be allowable to Applicants. Accordingly, reconsideration and allowance are requested.

If there are any additional charges with respect to this Amendment or otherwise, please charge them to Deposit Account No. 06-1130.

Respectfully submitted,

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